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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/825,012

DATE: 09/27/2001

TIME: 14:52:56

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\09272001\I825012.raw

ENTERED

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3 <110> APPLICANT: Young, Robert
5 <120> TITLE OF INVENTION: Compounds for Targeting
7 <130> FILE REFERENCE: 43191-256808
9 <140> CURRENT APPLICATION NUMBER: US 09/825,012
10 <141> CURRENT FILING DATE: 2001-04-03
12 <150> PRIOR APPLICATION NUMBER: US 60/237,159
13 <151> PRIOR FILING DATE: 2000-10-02
15 <150> PRIOR APPLICATION NUMBER: GB 0008049.9
16 <151> PRIOR FILING DATE: 2000-04-03
18 <160> NUMBER OF SEQ ID NOS: 102
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 282
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
29 Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
30 1 5 10 15
33 Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
34 20 25 30
37 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
38 35 40 45
41 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
42 50 55 60
45 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
46 65 70 75 80
49 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
50 85 90 95
53 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
54 100 105 110
57 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
58 115 120 125
61 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
62 130 135 140
65 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
66 145 150 155 160
69 Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
70 165 170 175
73 Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
74 180 185 190
77 Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
78 195 200 205
81 Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
82 210 215 220
85 Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
86 225 230 235 240
89 Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn

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90          245          250          255
93 Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
94          260          265          270
97 Asp His Tyr Pro Val Glu Val Met Leu Lys
98          275          280
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 1039
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 2
107 tcctgcacag gcagtgcctt gaagtgcctt ttcagagacc tttcttcata gactactttt      60
109 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag      120
111 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg      180
113 ggggcgctgc tggcactggc ggcoctactg cagggggcgc tgtccctgaa gatcgagcc      240
115 ttoaacatcc agacatttgg ggagaccaag atgtccaatg ccacctctgt cagctacatt      300
117 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg      360
119 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac      420
121 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg      480
123 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg      540
125 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc      600
127 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac      660
129 gctctctatg acgtctacct ggatgtocaa gagaaatggg gcttggagga cgtcatgttg      720
131 atgggcgact tcaatgcggg ctgcagctat gtgagacctt cccagtggtc atccatccgc      780
133 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca      840
135 cccacgcact gtgcctatga caggatcgct gttgcaggga tgctgctccg aggcgcggtt      900
137 gttcccgaact cggctcttcc ctttaacttc cagggtgcct atggcctgag tgaccaactg      960
139 gcccagcca tcaagtacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc     1020
141 cacaccagtt gaactgcag                                     1039
144 <210> SEQ ID NO: 3
145 <211> LENGTH: 260
146 <212> TYPE: PRT
147 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 3
151 Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met
152 1          5          10          15
155 Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr
156          20          25          30
159 Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val
160          35          40          45
163 Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His
164          50          55          60
167 Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr
168 65          70          75          80
171 Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr
172          85          90          95
175 Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu
176          100          105          110
179 Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe
180          115          120          125

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183 Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
184      130                      135                      140
187 Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu
188 145                      150                      155                      160
191 Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val
192                      165                      170                      175
195 Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe
196                      180                      185                      190
199 Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His
200                      195                      200                      205
203 Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala
204      210                      215                      220
207 Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly
208 225                      230                      235                      240
211 Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu
212                      245                      250                      255
215 Val Met Leu Lys
216      260

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219 &lt;210&gt; SEQ ID NO: 4

220 &lt;211&gt; LENGTH: 783

221 &lt;212&gt; TYPE: DNA

222 &lt;213&gt; ORGANISM: Homo sapiens

224 &lt;400&gt; SEQUENCE: 4

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225 ctgaagatcg cagccttcaa catccagaca tttggggaga ccaagatgtc caatgccacc      60
227 ctgcgtcagct acattgtgca gatcctgagc cgctacgaca tcgccctggt ccaggaggtc      120
229 agagacagcc acctgactgc cgtggggaag ctgctggaca acctcaatca ggacgcacca      180
231 gacacctatc actacgtggt cagtgaacca ctgggacgga acagctataa ggagcgctac      240
233 ctgttcgtgt acaggcctga ccaggtgtct gcggtggaca gctactacta cgatgatggc      300
235 tgcgagccct gcggaacga caccttcaac cgagagccag ccattgtcag gttcttctcc      360
237 cggttcacag aggtcagga gtttgccatt gtccocctgc atgcggcccc gggggacgca      420
239 gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaagagaa atggggcttg      480
241 gaggacgtca tgttgatggg cgacttcaat gcgggotgca gctatgtgag accctcccag      540
243 tggtcaccca tccgcctgtg gacaagcccc acctccagt ggctgatccc cgacagcgct      600
245 gacaccacag ctacacccac gcaactgtgcc tatgacagga tcgtggttgc agggatgctg      660
247 ctccgagggg ccgttggttc cgactcggct cttcccttta acttcaggc tgcctatggc      720
249 ctgagtgacc aactggccca agccatcagt gaccactatc cagtggaggt gatgctgaag      780
251 tga

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254 &lt;210&gt; SEQ ID NO: 5

255 &lt;211&gt; LENGTH: 161

256 &lt;212&gt; TYPE: PRT

257 &lt;213&gt; ORGANISM: Homo sapiens

259 &lt;400&gt; SEQUENCE: 5

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261 Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
262 1      5      10      15
265 Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
266      20      25      30
269 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
270      35      40      45
273 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp

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274      50      55      60
277 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
278 65      70      75      80
281 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
282      85      90      95
285 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
286      100      105      110
289 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
290      115      120      125
293 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
294      130      135      140
297 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
298 145      150      155      160
301 Asp
305 <210> SEQ ID NO: 6
306 <211> LENGTH: 858
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 6
311 gccgccacca tgaggggcat gaagctgctg ggggcgctgc tggcactggc ggccctactg      60
313 cagggggccg tgtccctgaa gatcgagcc ttcaacatcc agacatttgg ggagaccaag      120
315 atgtccaatg ccaccctcgt cagctacatt gtgcagatcc tgagccgcta cgacatcgcc      180
317 ctggtccagc aggtcagaga cagccacctg actgccgtgg ggaagctgct ggacaacctc      240
319 aatcaggacg caccagacac ctatcactac gtggtcagtg agccactggg acggaacagc      300
321 tataaggagc gctacctgtt cgtgtacagg cctgaccagg tgtctgcggg ggacagctac      360
323 tactacgatg atggctgcga gccctgcggg aacgacacct tcaaccgaga gccagccatt      420
325 gtcaggttct tctcccgggt cacagaggtc agggagtgtg ccattgttcc cctgcatgcg      480
327 gccccggggg acgcagtagc cgagatcgac gctctctatg acgtctacct ggatgtccaa      540
329 gagaaatggg gcttggagga cgtcatgttg atgggcgact tcaatgcggg ctgcagctat      600
331 gtgagaccct ccagtggtc atccatccgc ctgtggacaa gcccacctt ccagtggtg      660
333 atccccgaca gcgctgacac cacagctaca ccacgcact gtgcctatga caggatcgtg      720
335 gttgcaggga tgctgctccg aggggccgtt gttcccgaact cggtcttcc ctttaacttc      780
337 caggctgcct atggcctgag tgaccaactg gcccaagcca tcagtgaacca ctatccagtg      840
339 gaggtgatgc tgaagtga
342 <210> SEQ ID NO: 7
343 <211> LENGTH: 721
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
348 <223> OTHER INFORMATION: Humanised HMFG-1 light chain
350 <400> SEQUENCE: 7
351 atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactccgac      60
353 atccagatga ccagagccc aagcagcctg agcgccagcg tgggtgacag agtgaccatc      120
355 acctgtaagt ccagtcagag ccttttatat agtagcaatc aaaagatcta cttggcctgg      180
357 taccagcaga agccaggtaa ggctccaaag ctgctgatct actgggcata cactagggaa      240
359 tctggtgtgc caagcagatt cagcggtagc ggtagcggta ccgacttcac cttcaccatc      300
361 agcagcctcc agccagagga catcgccacc tactactgcc agcaatatta tagatatcct      360
363 cggacgttcg gccaaaggga caaggtggaa atcaaacgaa ctgtggctgc accatctgtc      420
365 ttcattcttc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgctg      480

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367 ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 540
369 tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 600
371 agcagcaccg tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 660
373 gtcacccatc agggcctgag ctgcccgcgc acaaagagct tcaacagggg agagtgttag 720
375 a 721

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378 &lt;210&gt; SEQ ID NO: 8

379 &lt;211&gt; LENGTH: 730

380 &lt;212&gt; TYPE: DNA

381 &lt;213&gt; ORGANISM: Artificial Sequence

383 &lt;220&gt; FEATURE:

384 &lt;223&gt; OTHER INFORMATION: Humanised HMFG-1 light chain

386 &lt;400&gt; SEQUENCE: 8

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387 gccgccacca tgggatggag ctgtatcatc ctcttcttgg tagcaacagc tacaggtgtc 60
389 cactccgaca tccagatgac ccagagccca agcagoccta gcgccagcgt gggtgacaga 120
391 gtgaccatca cctgtaagtc cagtcagagc cttttatata gtagcaatca aaagatctac 180
393 ttggcctggg accagcagaa gccaggtaag gtcctaaagc tgcctgatcta ctgggcatcc 240
395 actaggggaat ctggtgtgcc aagcagattc agcggtagcg gtacgggtac cgacttcacc 300
397 ttcaccatca gcagcctcca gccagaggac atcgccacct actactgcca gcaatattat 360
399 agatatcctc ggacgttcgg ccaagggacc aaggtggaaa tcaaacgaac tgtggctgca 420
401 ccactctgtc tcactctccc gccatctgat gagcagttga aatctggaac tgcctctgtt 480
403 gtgtgcctgc tgaataactt ctatccaga gaggccaaag tacagtggaa ggtggataac 540
405 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
407 tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
409 gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720
411 gagtgttaga 730

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414 &lt;210&gt; SEQ ID NO: 9

415 &lt;211&gt; LENGTH: 239

416 &lt;212&gt; TYPE: PRT

417 &lt;213&gt; ORGANISM: Artificial Sequence

419 &lt;220&gt; FEATURE:

420 &lt;223&gt; OTHER INFORMATION: Humanised HMFG-1 light chain

422 &lt;400&gt; SEQUENCE: 9

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424 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
425 1 5 10 15
428 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
429 20 25 30
432 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu
433 35 40 45
436 Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys
437 50 55 60
440 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
441 65 70 75 80
444 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
445 85 90 95
448 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
449 100 105 110
452 Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gln Gly Thr Lys
453 115 120 125
456 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro

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VERIFICATION SUMMARY

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